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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- 5
- (i) APPLICANT: HOWARD FLOREY INSTITUTE OF  
EXPERIMENTAL PHYSIOLOGY AND MEDICINE  
MENDELSON, FRED  
CHAI, SIEW YEEN  
10 MOELLER, INGRID  
ALDRED, PETER  
SMITH, IAN A  
LEW, REBECCA A
- 15 (ii) TITLE OF INVENTION: NEUROACTIVE PEPTIDE
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
- 20 (A) ADDRESSEE: GRIFFITH HACK  
(B) STREET: 509 ST KILDA ROAD  
(C) CITY: MELBOURNE  
(D) STATE: VICTORIA  
(E) COUNTRY: AUSTRALIA  
25 (F) ZIP: 3004
- (v) COMPUTER READABLE FORM:
- 30 (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version  
#1.30
- 35 (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: AU P00893  
(B) FILING DATE: 09-JUL-1996  
(C) CLASSIFICATION:
- 40 (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: SANTER, VIVIEN B  
(C) REFERENCE/DOCKET NUMBER: P21154
- (ix) TELECOMMUNICATION INFORMATION:
- 45 (A) TELEPHONE: +61 3 9243 8300  
(B) TELEFAX: +61 3 9243 8333/4

"Sequence Listing"

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B1

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## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

10

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

15

## (v) FRAGMENT TYPE: internal

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Leu Val Val Thr Pro Thr Thr Gly Ala Pro  
1 5

10

25

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

35

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

40

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

45

CTGGTTGTCT ACCCCTGGAC TCAGAG  
26

66E750"06H24T60

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B1  
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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

15 (v) FRAGMENT TYPE: internal

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTGAGTCC AGGGGTAGAC AACCAG  
26

25 (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

40 (v) FRAGMENT TYPE: internal

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTCAGGATCC ACATGCAGCT TATCACAG  
28

Sequence data

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## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

10

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: YES

15

## (v) FRAGMENT TYPE: internal

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAGCACAACC ACTAGCAT TGCC  
24

## 25 (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 1244 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

35

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

40

## (v) FRAGMENT TYPE: not applicable

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CACAAACTCA GAAACAGACA CCATGGTGCA CCTGAGTGCT TCTGACATAG  
TTGTGTTGAC 60

50 TCACAAACTC AGAAACAGAC ACCATGGTGC ACCTGACTGA TGCTGAGAAG  
GCTGCTGTTA 120

Sequence "divided"

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ATGGCCTGTG GGGAAAGGTG AACCTGATG ATGTTGGCTG ATGCTGAGAA  
 GGCTGCTGTT 180

5 AATGGCCTGT GGGGAAAGGT GAACCCTGAT GATGTTGGTG GCGAGGCCCT  
 GGGCAGGCTG 240

CTGGTTGTCT ACCCTTGGAC CCAGAGGTAC TTTGATAGGT GGCGAGGCCC  
 TGGGCAGGCT 300

10 GCTGGTTGTC TACCCTTGGG CCCAGAGGTA CTTTGATAGC TTTGGGGACC  
 TGTCTCTGTC 360

CTCTGCTATC ATGGGTAACC CTAAGGTGAA GGCCCATGGG CTTTGGGGAC  
 CTGTCCTCTG 420

15 CCTCTGCTAT CATGGGTAAC CCTAAGGTGA AGGCCCATGG CAAGAAGGTG  
 ATAAACGCCT 480

TCAATGATGG CCTGAAACAC TTGGACAACC TCAAGGGCAG GCAAGAAGGT  
 20 GATAAACGCC 540

TTCAATGATG GCCTGAAACA CTTGGACAAC CTCAAGGGCA CCTTTGCTCA  
 TCTGAGTGAA 600

25 CTCCACTGTG ACAAGCTGCA TGTGGATCCT GAGAACTTCA GCCTTTGCTC  
 ATCTGAGTGA 660

ACTCCACTGT GACAAGCTGC ATGTGGATCC TGAGAACTTC AGGCTCCTGG  
 30 GCAATATGAT 720

TGTGATTGTG TTGGGCCACC ACCTGGGCAA GGAATTCACC CGGGCTCCTG  
 GGCAATATGA 780

TTGTGATTGT GTTGGGCCAC CACCTGGGCA AGGAATTCAC CCCCTGTGCA  
 35 CAGGCTGCCT 840

TCCAGAAGGT GGTGGCTGGA GTGGCCAGTG CCCTGGCTCA CAGCCTGTGC  
 ACAGGCTGCC 900

40 TTCCAGAAGG TGGTGGCTGG AGTGGCCAGT GCCCTGGCTC ACAAGTACCA  
 CTAAACCTCT 960

TTTCTGCTC TTGTCTTTGT GCAATGGTCA ATTGTTCCCA AGAGAGTACC  
 45 ACTAAACCTC 1020

TTTTCTGCT CTTGTCTTTG TGCAATGGTC AATTGTTCCC AAGAGAGCAT  
 CTGTCAGTTG 1080

TTGTCAAAAT GACAAAGACC TTTGAAAATC TGTCTACTA ATAAGGAGCA  
 50 TCTGTCAGTT 1140

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GTTGTCAAAA TGACAAAGAC CTTTGAAAAT CTGTCCTACT AATAAAAGGC  
ATTTACTTTC 1200

5 ACTGCAAAAA AAAAAAAAAA AAAGAAGGCA TTTACTTTCA CTGC  
1244

(2) INFORMATION FOR SEQ ID NO:7:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 649 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

25 CACAACTCA GAAACAGACA CCATGGTGCA CCTGACTGAT GCTGAGAAGG  
CTGCTGTTAA 60

TGGCCTGTGG GGAAAGGTGA ACCCTGATGA TGTGTAAAG GGTGGCGAGG  
CCCTGGGCAG 120

30 GCTGCTGGTT GTCTACCCTT GGACCCAGAG GTACTTTGAT AGGAGTGCTT  
TGGGGACCTG 180

TCCTCTGCCT CTGCTATCAT GGGTAACCCT AAGGTGAAGG CCCATGGAAG  
AGCAAGAAGG 240

35 TGATAAACGC CTTCAATGAT GGCCTGAAAC ACTTGACAA CCTCAAGGGC  
AGAGGCCTTT 300

40 GCTCATCTGA GTGAACTCCA CTGTGACAAG CTGCATGTGG ATCCTGAGAA  
CTTCATACGG 360

CTCCTGGGCA ATATGATTGT GATTGTGTTG GGCCACCACC TGGGCAAGGA  
ATTCACCCGG 420

45 GTCCTGTGCA CAGGCTGCCT TCCAGAAGGT GGTGGCTGGA GTGGCCAGTG  
CCCTGGCTCA 480

CACAAAAGAA AAGTACCACT AAACCTCTTT TCCTGCTCTT GTCTTTGTGC  
AATGGTCAAT 540

50 TGTTCCCAAG AGAGCATCTG TCAGTTGTTG TCAAAATGAC AAAGACCTTT  
GAAAATCTGT 600

Sequence

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cont

CCTACTAATA AAAGGCATTT ACTTTCCTG CAAAAAAAAA AAAAAAAAAA  
649

Seq  
B1  
cont

Seq B1 cont